

## SEQUENCE LISTING

<110> Xu, Wenfeng  
 Kindsvogel, Wayne  
 Chandrasekher, Yasmin A.  
 Dillon, Stacey R.  
 Lehner, Joyce M.  
 Siadak, Anthony W.  
 Sivakumar, Pallavur V.  
 Moore, Margaret D.

<120> ANTI-IL-22RA ANTIBODIES AND BINDING  
 PARTNERS AND METHODS OF USING IN INFLAMMATION

<130> 03-02

<150> US 60/457,481

<151> 2003-03-24

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<151> 2003-11-17

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Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys
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Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
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Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
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His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
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Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
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Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
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325    330    335
Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
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Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
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Lys	Glu	Ser	Ala	Pro	Tyr	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg
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Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile
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Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro
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His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro
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Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala
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Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu
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Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
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 Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu  
 80 85 90  
 atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341  
 Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln  
 95 100 105  
 tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389  
 Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala  
 110 115 120  
 agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437  
 Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu  
 125 130 135  
 cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485  
 His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu  
 140 145 150 155  
 gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533  
 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe  
 160 165 170  
 atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587  
 Met Ser Leu Arg Asn Ala Cys Ile  
 175  
 taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647

```

aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707
tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag acttttctaag 767
catagatatt tattgataac atttcattgt aactgggtgt ctatacacag aaaacaattt 827
atTTTTTaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887
aaaccctaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat 947
tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa 1007
acatcattcg atattgctac ttgagtgtaa ggctaataatt gatatttatg acaataatta 1067
tagagctata acatgtttat ttgacctcaa taaacacttg gatatccta 1116

```

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<210> 6
<211> 179
<212> PRT
<213> Homo sapiens

```

```

<400> 6
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
1      5      10      15
Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
20     25     30
Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
35     40     45
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
50     55     60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65     70     75     80
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
85     90     95
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
100    105    110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
115    120    125
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
130    135    140
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145    150    155    160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
165    170    175
Ala Cys Ile

```

```

<210> 7
<211> 926
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (45)...(575)
<221> variation
<222> (188)...(188)
<223> Nucleotide may be C or G at position 188

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<400> 7
ctttgaattc ctagctcctg tggctctccag atttcaggcc taag atg aaa gcc tct 56
                                Met Lys Ala Ser
                                1

agt ctt gcc ttc agc ctt ctc tct gct gcg ttt tat ctc cta tgg act 104
Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
5      10      15      20

cct tcc act gga ctg aag aca ctc aat ttg gga agc tgt gtg atc gcc 152
Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile Ala
25      30      35

```



```

aca aac ctt cag gaa ata cga aat gga ttt tct gas ata cgg ggc agt      200
Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa Ile Arg Gly Ser
          40                      45                      50

gtg caa gcc aaa gat gga aac att gac atc aga atc tta agg agg act      248
Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu Arg Arg Thr
          55                      60                      65

gag tct ttg caa gac aca aag cct gcg aat cga tgc tgc ctc ctg cgc      296
Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys Cys Leu Leu Arg
          70                      75                      80

cat ttg cta aga ctc tat ctg gac agg gta ttt aaa aac tac cag acc      344
His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys Asn Tyr Gln Thr
          85                      90                      95                      100

cct gac cat tat act ctc cgg aag atc agc agc ctc gcc aat tcc ttt      392
Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu Ala Asn Ser Phe
          105                      110                      115

ctt acc atc aag aag gac ctc cgg ctc tgt cat gcc cac atg aca tgc      440
Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala His Met Thr Cys
          120                      125                      130

cat tgt ggg gag gaa gca atg aag aaa tac agc cag att ctg agt cac      488
His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln Ile Leu Ser His
          135                      140                      145

ttt gaa aag ctg gaa cct cag gca gca gtt gtg aag gct ttg ggg gaa      536
Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys Ala Leu Gly Glu
          150                      155                      160

cta gac att ctt ctg caa tgg atg gag gag aca gaa tag gaggaagtg      585
Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu *
          165                      170                      175

atgctgctgc taagaatatt cgagggtcaag agctccagtc ttcaataacct gcagaggagg      645
catgacccca aaccaccatc tctttactgt actagtcttg tgctgggtcac agtgtatctt      705
atztatgcat tacttgcttc cttgcatgat tgtctttatg catccccaat cttaattgag      765
accatacttg tataagattt ttgtaatatc tttctgctat tggatatatt tattagttaa      825
tatatttatt tattttttgc tattaatgta ttttaatttt tacttgggca tgaaacttta      885
aaaaaaattc acaagattat atttataacc tgactagagc a                               926

<210> 8
<211> 176
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (48)...(48)
<223> Amino acid at position 48 can be a D (Asp) or E
      (Glu)

<221> VARIANT
<222> 48
<223> Xaa = Any Amino Acid

<400> 8
Met Lys Ala Ser Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr
  1      5      10      15
Leu Leu Trp Thr Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser
  20      25      30
Cys Val Ile Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa
  35      40      45

```

```

Ile Arg Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile
 50      55      60
Leu Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
65      70      75      80
Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys
      85      90      95
Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu
      100      105      110
Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala
      115      120      125
His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln
      130      135      140
Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys
145      150      155      160
Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu
      165      170      175

```

```

<210> 9
<211> 16
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Peptide Linker

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<400> 9
Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1          5          10          15

```

```

<210> 10
<211> 1050
<212> DNA
<213> Mus musculus

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```

<220>
<221> CDS
<222> (5)...(589)

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<400> 10
aaca ggc tct cct ctc act tat caa ctt ttg aca ctt gtg cga tcg gtg      49
  Gly Ser Pro Leu Thr Tyr Gln Leu Leu Thr Leu Val Arg Ser Val
  1          5          10          15

atg gct gtc ctg cag aaa tct atg agt ttt tcc ctt atg ggg act ttg      97
Met Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu
      20          25          30

gcc gcc agc tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat      145
Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn
      35          40          45

gcg ctg ccc atc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag      193
Ala Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
      50          55          60

cag ccg tac atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc      241
Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
      65          70          75

ctt gca gat aac aac aca gac gtc cgg ctc atc ggg gag aaa ctg ttc      289
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
      80          85          90          95

cga gga gtc agt gct aag gat cag tgc tac ctg atg aag cag gtg ctc      337

```

Arg	Gly	Val	Ser	Ala	Lys	Asp	Gln	Cys	Tyr	Leu	Met	Lys	Gln	Val	Leu		
				100					105					110			
aac	ttc	acc	ctg	gaa	gac	att	ctg	ctc	ccc	cag	tca	gac	agg	ttc	cgg		385
Asn	Phe	Thr	Leu	Glu	Asp	Ile	Leu	Leu	Pro	Gln	Ser	Asp	Arg	Phe	Arg		
			115					120					125				
ccc	tac	atg	cag	gag	gtg	gtg	cct	ttc	ctg	acc	aaa	ctc	agc	aat	cag		433
Pro	Tyr		Gln	Glu	Val	Val	Pro	Phe	Leu	Thr	Lys	Leu	Ser	Asn	Gln		
		130					135					140					
ctc	agc	tcc	tgt	cac	atc	agt	ggg	gac	gac	cag	aac	atc	cag	aag	aat		481
Leu	Ser	Ser	Cys	His	Ile	Ser	Gly	Asp	Asp	Gln	Asn	Ile	Gln	Lys	Asn		
	145					150					155						
gtc	aga	agg	ctg	aag	gag	aca	gtg	aaa	aag	ctt	gga	gag	agc	gga	gag		529
Val	Arg	Arg	Leu	Lys	Glu	Thr	Val	Lys	Lys	Leu	Gly	Glu	Ser	Gly	Glu		
160					165					170					175		
atc	aaa	gcg	atc	ggg	gaa	ctg	gac	ctg	ctg	ttt	atg	tct	ctg	aga	aat		577
Ile	Lys	Ala	Ile	Gly	Glu	Leu	Asp	Leu	Leu	Phe	Met	Ser	Leu	Arg	Asn		
				180					185					190			
gct	tgc	gtc	tga	gcgagaagaa	gctagaaaac	gaagaactgc	tccttcctgc										629
Ala	Cys	Val	*														

cttctaaaaa	gaacaataag	atccctgaat	ggactttttt	actaaaggaa	agtgagaagc		689
taacgtccac	catcattaga	agatttcaca	tgaacacctg	ctcagttgaa	agagaaaata		749
gtgtcaagtt	gtccatgaga	ccagaggtag	acttgataac	cacaaagatt	cattgacaat		809
atattattgt	cattgataat	gcaacagaaa	aagtatgtac	tttaaaaaat	tgtttgaaag		869
gaggttacct	ctcattcctc	tagaagaaaa	gcctatgtaa	cttcattttcc	ataaccaata		929
ctttatatat	gtaagtttat	ttattataag	tatacatatt	atttatgtca	gtttattaat		989
atggatttat	ttatagaaaa	attatctgat	gttgatattt	gagtataaag	caaataatat		1049
t							1050

<210> 11  
 <211> 194  
 <212> PRT  
 <213> Mus musculus

<400> 11																	
Gly	Ser	Pro	Leu	Thr	Tyr	Gln	Leu	Leu	Thr	Leu	Val	Arg	Ser	Val	Met		
1				5					10					15			
Ala	Val	Leu	Gln	Lys	Ser	Met	Ser	Phe	Ser	Leu	Met	Gly	Thr	Leu	Ala		
			20					25					30				
Ala	Ser	Cys	Leu	Leu	Leu	Ile	Ala	Leu	Trp	Ala	Gln	Glu	Ala	Asn	Ala		
		35					40					45					
Leu	Pro	Ile	Asn	Thr	Arg	Cys	Lys	Leu	Glu	Val	Ser	Asn	Phe	Gln	Gln		
	50					55					60						
Pro	Tyr	Ile	Val	Asn	Arg	Thr	Phe	Met	Leu	Ala	Lys	Glu	Ala	Ser	Leu		
65				70					75					80			
Ala	Asp	Asn	Asn	Thr	Asp	Val	Arg	Leu	Ile	Gly	Glu	Lys	Leu	Phe	Arg		
				85					90					95			
Gly	Val	Ser	Ala	Lys	Asp	Gln	Cys	Tyr	Leu	Met	Lys	Gln	Val	Leu	Asn		
			100					105					110				
Phe	Thr	Leu	Glu	Asp	Ile	Leu	Leu	Pro	Gln	Ser	Asp	Arg	Phe	Arg	Pro		
		115				120						125					
Tyr	Met	Gln	Glu	Val	Val	Pro	Phe	Leu	Thr	Lys	Leu	Ser	Asn	Gln	Leu		
	130					135					140						
Ser	Ser	Cys	His	Ile	Ser	Gly	Asp	Asp	Gln	Asn	Ile	Gln	Lys	Asn	Val		
145				150					155					160			
Arg	Arg	Leu	Lys	Glu	Thr	Val	Lys	Lys	Leu	Gly	Glu	Ser	Gly	Glu	Ile		
				165					170					175			
Lys	Ala	Ile	Gly	Glu	Leu	Asp	Leu	Leu	Phe	Met	Ser	Leu	Arg	Asn	Ala		
			180					185					190				

Cys Val

<210> 12  
 <211> 2149  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(693)

<400> 12  
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 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
 1 5 10 15  
 act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag 96  
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
 20 25 30  
 agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag 144  
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
 35 40 45  
 cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac 192  
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
 50 55 60  
 aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt 240  
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
 65 70 75 80  
 act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag 288  
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
 85 90 95  
 gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca 336  
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
 100 105 110  
 gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata 384  
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
 115 120 125  
 gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta 432  
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
 130 135 140  
 att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat 480  
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
 145 150 155 160  
 gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att 528  
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
 165 170 175  
 aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga 576  
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
 180 185 190  
 gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg 624  
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
 195 200 205

gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa 672  
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
 210 215 220

gag aga tgt gtg gaa att cca tgacttgtgg aatttggcat tcagcaatgt 723  
 Glu Arg Cys Val Glu Ile Pro  
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtgtt tgaaggatct tattttaaatt 783  
 tgtttttgta ttttctttaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843  
 ccattctttt atcctttata tttcatttta aactatattt gaacgacatt cccccgaaa 903  
 aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aactttattt 963  
 ctgaatgtaa catccctaata aacaaccttc attcttctaa tacagcaaaa taaaaattta 1023  
 acaaccaagg aatagtattt aagaaaatgt tgaaataatt tttttaaatt agcattacag 1083  
 actgaggcgg tcctgaagca atgggtttttc actctcttat tgagccaatt aaattgacat 1143  
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 tgaatatact ttttatatat ttattattat taaatatattt tacttaattga atcaaaattt 1263  
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 acaaagaaga aaggaaacct cattactcaa tccttctggc caagagtgtc ttgcttgttg 1563  
 cgccttcttc atctctatat aggaggatcc catgaatgat ggtttatttg gaactgctgg 1623  
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 gccccctctg ctactgcct ctctgagta gaaatctggt gacctaaagg tcagtgcggt 1803  
 caacagaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgcctt 1863  
 tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa 1923  
 agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagt ataatggat 1983  
 taaaaaatat tcagaaatgt attggggggt ggaggagaat aagaggcaga gcaagagcta 2043  
 gagaattggt ttccttgctt ccctgtatgc tcagaaaaca ttgatttgag catagacgca 2103  
 gagactgaaa aaaaaaaaaa gctcgagcgg cgcgcataatc cttggt 2149

<210> 13  
 <211> 231  
 <212> PRT  
 <213> Homo sapiens

<400> 13  
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
 1 5 10  
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
 20 25 30  
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
 35 40 45  
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
 50 55 60  
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
 65 70 75 80  
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
 85 90 95  
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
 100 105 110  
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
 115 120 125  
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
 130 135 140  
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
 145 150 155 160  
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
 165 170 175  
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
 180 185 190  
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
 195 200 205  
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu

210 215  
 Glu Arg Cys Val Glu Ile Pro  
 225 230

220

<210> 14  
 <211> 699  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> C-Terminal Fc4 tag

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 ggggacaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120  
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180  
 aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 240  
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300  
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360  
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420  
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480  
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540  
 cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600  
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660  
 tacacgcaga agagcctctc cctgtctccg ggtaaataa 699

<210> 15  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Glu-Glu (CEE) Peptide Tag

<400> 15  
 Glu Tyr Met Pro Met Glu  
 1 5

<210> 16  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Glu-Glu (CEE) Peptide Tag with spacer

<400> 16  
 Gly Ser Gly Gly Glu Tyr Met Pro Met Glu  
 1 5 10

<210> 17  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC39289

<400> 17  
 tccgaggagt caatgctaag 20

<210> 18  
 <211> 20

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer ZC39290  
  
 <400> 18  
 tccaagcttt ttcactgtct 20  
  
 <210> 19  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer ZC39776  
  
 <400> 19  
 gggcccgcta gcacct 16  
  
 <210> 20  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Primer ZC39777  
  
 <400> 20  
 gggatgatccg ctggca 16  
  
 <210> 21  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> IL-20 FAM/TAMRA labeled TaqMan probe ZC38752  
  
 <400> 21  
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 <223> reverse primer, ZC40542  
  
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 <223> Oligonucleotide primer ZC45,593  
  
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 Leu Leu Trp Thr Pro Leu Thr Gly Leu Lys Thr Leu His Leu Gly Ser  
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tgt gtg att act gca aac cta cag gca ata caa aag gaa ttt tct gag 144  
 Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu  
 35 40 45

att cgg gat agt gtg caa gct gaa gat aca aat att gac atc aga att 192  
 Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile  
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tta agg acg act gag tct ttg aaa gac ata aag tct ttg gat agg tgc 240  
 Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys  
 65 70 75 80

tgc ttc ctt cgt cat cta gtg aga ttc tat ctg gac agg gta ttc aaa 288  
 Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys  
 85 90 95

gtc tac cag acc cct gac cac cat acc ctg aga aag atc agc agc ctc 336  
 Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu  
 100 105 110

gcc aac tcc ttt ctt atc atc aag aag gac ctc tca gtc tgt cat tct 384  
 Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser  
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cac atg gca tgt cat tgt ggg gaa gaa gca atg gag aaa tac aac caa 432  
 His Met Ala Cys His Cys Gly Glu Glu Ala Met Glu Lys Tyr Asn Gln

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Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys			
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gct ttg gga gaa cta ggc att ctt ctg aga tgg atg gag gag atg cta			528
Ala Leu Gly Glu Leu Gly Ile Leu Leu Arg Trp Met Glu Glu Met Leu			
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tag			531
*			

<210> 33  
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 Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu  
 35 40 45  
 Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile  
 50 55 60  
 Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys  
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 Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys  
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 Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu  
 100 105 110  
 Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser  
 115 120 125  
 His Met Ala Cys His Cys Gly Glu Glu Ala Met Glu Lys Tyr Asn Gln  
 130 135 140  
 Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys  
 145 150 155 160  
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<210> 35  
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 <212> DNA  
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<220>  
 <223> Oligonucleotide primer ZC45039

<400> 35  
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<210> 36
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<212> DNA
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<220>
<223> Oligonucleotide primer ZC38573

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<210> 37
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<400> 37
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<210> 38
<211> 24
<212> DNA
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<220>
<223> Oligonucleotide primer ZC40128

<400> 38
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<210> 39
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<212> DNA
<213> Artificial Sequence

<220>
<223> IL-22RA Extracellular domain with tPA leader and
      fused to murine gamma 2a heavy chain Fc region
      (mG2a)

<221> CDS
<222> (1)...(1473)

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gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc   96
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
          20          25          30

ttc cgt aga cac gcc cct gag gac ccc tcg gat ctg ctc cag cac gtg   144
Phe Arg Arg His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val
          35          40          45

aaa ttc cag tcc agc aac ttt gaa aac atc ctg acg tgg gac agc ggg   192
Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly
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cca gag ggc acc cca gac acg gtc tac agc atc gag tat aag acg tac   240
Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr

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aag Lys	tcc Ser	tgc Cys	aac Asn 100	ctg Leu	acg Thr	gtg Val	gag Glu	acg Thr 105	ggc Gly	aac Asn	ctc Leu	acg Thr	gag Glu 110	ctc Leu	tac Tyr	336
tat Tyr	gcc Ala	agg Arg 115	gtc Val	acc Thr	gct Ala	gtc Val	agt Ser 120	gcg Ala	gga Gly	ggc Gly	cgg Arg	tca Ser 125	gcc Ala	acc Thr	aag Lys	384
atg Met	act Thr 130	gac Asp	agg Arg	ttc Phe	agc Ser	tct Ser 135	ctg Leu	cag Gln	cac His	act Thr	acc Thr 140	ctc Leu	aag Lys	cca Pro	cct Pro	432
gat Asp 145	gtg Val	acc Thr	tgt Cys	atc Ile	tcc Ser 150	aaa Lys	gtg Val	aga Arg	tcg Ser	att Ile 155	cag Gln	atg Met	att Ile	gtt Val	cat His 160	480
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cgc Arg	acc Thr	tac Tyr 195	caa Gln	atg Met	cac His	ctt Leu	gga Gly 200	ggg Gly	aag Lys	cag Gln	aga Arg	gaa Glu 205	tat Tyr	gag Glu	ttc Phe	624
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ggt Gly	gag Glu	ccc Pro	aga Arg 260	ggc Gly	ccc Pro	aca Thr	atc Ile	aag Lys 265	ccc Pro	tgt Cys	cct Pro	cca Pro	tgc Cys 270	aaa Lys	tgc Cys	816
cca Pro	gca Ala	cct Pro	aac Asn 275	ctc Leu	ttg Leu	ggt Gly	gga Gly 280	cca Pro	tcc Ser	gtc Val	ttc Phe	atc Ile 285	ttc Phe	cct Pro	cca Pro	864
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 His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn  
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 Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly  
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 Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Glu Glu Glu  
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 Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu  
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 aac tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac ttc 1344  
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 435 440 445  
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 Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn  
 450 455 460  
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 Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr  
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<210> 40

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-22RA Extracellular domain with tPA leader and  
fused to murine gamma 2a heavy chain Fc region  
(mG2a)

<400> 40

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 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg  
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 Phe Arg Arg His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val  
 35 40 45  
 Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly  
 50 55 60  
 Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr  
 65 70 75 80  
 Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg  
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 Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr  
 100 105 110

Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys  
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 Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro  
 130 135 140  
 Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His  
 145 150 155 160  
 Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu  
 165 170 175  
 Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn  
 180 185 190  
 Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe  
 195 200 205  
 Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys  
 210 215 220  
 Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys  
 225 230 235 240  
 Thr Leu Pro Asp Arg Thr Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser  
 245 250 255  
 Gly Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys  
 260 265 270  
 Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro  
 275 280 285  
 Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys  
 290 295 300  
 Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp  
 305 310 315 320  
 Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg  
 325 330 335  
 Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln  
 340 345 350  
 His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn  
 355 360 365  
 Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly  
 370 375 380  
 Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu  
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 Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met  
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 Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu  
 420 425 430  
 Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe  
 435 440 445  
 Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn  
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 Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
 485 490

<210> 41  
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 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (43)...(1788)

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 Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His Thr Thr Val Asp

5					10					15					20					
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tac Tyr	agt Ser	gtg Val 55	gaa Glu	tat Tyr	aag Lys	aaa Lys	tac Tyr 60	gga Gly	gag Glu	aga Arg	aag Lys	tgg Trp 65	ctg Leu	gcc Ala	aag Lys	246				
gcg Ala	ggc Gly 70	tgc Cys	cag Gln	cgg Arg	atc Ile	acc Thr 75	cag Gln	aag Lys	ttc Phe	tgc Cys	aac Asn 80	ctg Leu	act Thr	atg Met	gag Glu	294				
acc Thr 85	cgc Arg	aac Asn	cac His	act Thr	gag Glu 90	ttt Phe	tac Tyr	tac Tyr	gcc Ala	aag Lys 95	gtc Val	acg Thr	gca Ala	gtc Val	agc Ser 100	342				
gca Ala	gga Gly	ggc Gly	cca Pro	cca Pro 105	gtc Val	aca Thr	aag Lys	atg Met	act Thr 110	gat Asp	cgt Arg	ttc Phe	agc Ser	tcg Ser 115	ctg Leu	390				
cag Gln	cac His	act Thr 120	acc Thr	atc Ile	aaa Lys	ccg Pro	cct Pro	gat Asp 125	gtg Val	acc Thr	tgt Cys	atc Ile	ccc Pro 130	aaa Lys	gtg Val	438				
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ggc Gly	aaa Lys	cag Gln	aga Arg	gaa Glu 185	tac Tyr	gag Glu	ttc Phe	ctt Leu	ggc Gly 190	ctg Leu	act Thr	ccc Pro	gac Asp	aca Thr 195	gag Glu	630				
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Ser Ser Leu Pro Gln Pro Ile Gln Tyr Ser Gln Val Val Val Ser Gly	
295 300 305	
ccc agg gag cct cct gga gct gtg tgg cgg cag agc ctg tct gac ctc	1014
Pro Arg Glu Pro Pro Gly Ala Val Trp Arg Gln Ser Leu Ser Asp Leu	
310 315 320	
acc tac gta ggg cag tca gat gtc tcc atc ctg caa cct acc aac gtg	1062
Thr Tyr Val Gly Gln Ser Asp Val Ser Ile Leu Gln Pro Thr Asn Val	
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cca gct cag cag aca ctg tcc cca cca tcc tac gct ccg aag gct gtc	1110
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345 350 355	
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Pro Glu Val Gln Pro Pro Ser Tyr Ala Pro Gln Val Ala Ser Asp Ala	
360 365 370	
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Lys Ala Leu Phe Tyr Ser Pro Gln Gln Gly Met Lys Thr Arg Pro Ala	
375 380 385	
acc tat gac ccg cag gac att ctg gac agc tgc cct gct tct tat gct	1254
Thr Tyr Asp Pro Gln Asp Ile Leu Asp Ser Cys Pro Ala Ser Tyr Ala	
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425 430 435	
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Val Arg Ser Cys Leu Pro Gly Asp Leu Ser Leu Gln Lys Val Thr Ser	
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Glu Pro Glu Thr Pro Arg Tyr Leu Lys Gly Ala Leu Ser Leu Leu Ser	
485 490 495 500	
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505 510 515	
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Leu Asp Ser Leu Val Cys Pro Lys Asp Glu Gly Pro Ala Val Glu Thr	



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Glu	Leu	Asp	Ser	Leu	Phe	Lys	Gly	Leu	Ala	Leu	Thr	Val	Gln	Trp	Glu	
565					570					575					580	
tcc	tga	agggagatcg	gagcaagcag gcctaagttt cctccccgcc										caccta	1834		
Ser	*															

<210> 42  
 <211> 581  
 <212> PRT  
 <213> Mus musculus

<400> 42

Met	Lys	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His
1				5					10				15		
Thr	Thr	Val	Asp	Thr	Ser	Gly	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser
			20				25					30			
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Gly	Gly	Pro	Ala	Ser	Thr
		35				40					45				
Ser	Asp	Thr	Val	Tyr	Ser	Val	Glu	Tyr	Lys	Lys	Tyr	Gly	Glu	Arg	Lys
	50					55					60				
Trp	Leu	Ala	Lys	Ala	Gly	Cys	Gln	Arg	Ile	Thr	Gln	Lys	Phe	Cys	Asn
65					70					75					80
Leu	Thr	Met	Glu	Thr	Arg	Asn	His	Thr	Glu	Phe	Tyr	Tyr	Ala	Lys	Val
				85					90					95	
Thr	Ala	Val	Ser	Ala	Gly	Gly	Pro	Pro	Val	Thr	Lys	Met	Thr	Asp	Arg
			100				105					110			
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Ile	Lys	Pro	Pro	Asp	Val	Thr	Cys
		115				120						125			
Ile	Pro	Lys	Val	Arg	Ser	Ile	Gln	Met	Leu	Val	His	Pro	Thr	Leu	Thr
	130					135					140				
Pro	Val	Leu	Ser	Glu	Asp	Gly	His	Gln	Leu	Thr	Leu	Glu	Glu	Ile	Phe
145					150					155					160
His	Asp	Leu	Phe	Tyr	Arg	Leu	Glu	Leu	His	Val	Asn	His	Thr	Tyr	Gln
			165						170					175	
Met	His	Leu	Glu	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Leu	Gly	Leu	Thr
		180						185					190		
Pro	Asp	Thr	Glu	Phe	Leu	Gly	Ser	Ile	Thr	Ile	Leu	Thr	Pro	Ile	Leu
		195					200					205			
Ser	Lys	Glu	Ser	Ala	Pro	Tyr	Val	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp
	210					215					220				
Arg	Thr	Trp	Ala	Tyr	Ser	Phe	Ser	Gly	Ala	Val	Leu	Phe	Ser	Met	Gly
225					230					235					240
Phe	Leu	Val	Gly	Leu	Leu	Cys	Tyr	Leu	Gly	Tyr	Lys	Tyr	Ile	Thr	Lys
			245						250					255	
Pro	Pro	Val	Pro	Pro	Asn	Ser	Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe
		260						265					270		
Gln	Pro	Leu	Arg	Phe	Ile	Gln	Glu	His	Val	Leu	Ile	Pro	Val	Leu	Asp
		275					280					285			
Leu	Ser	Gly	Pro	Ser	Ser	Leu	Pro	Gln	Pro	Ile	Gln	Tyr	Ser	Gln	Val
	290					295					300				
Val	Val	Ser	Gly	Pro	Arg	Glu	Pro	Pro	Gly	Ala	Val	Trp	Arg	Gln	Ser
305					310					315					320
Leu	Ser	Asp	Leu	Thr	Tyr	Val	Gly	Gln	Ser	Asp	Val	Ser	Ile	Leu	Gln
			325						330					335	
Pro	Thr	Asn	Val	Pro	Ala	Gln	Gln	Thr	Leu	Ser	Pro	Pro	Ser	Tyr	Ala
		340						345					350		
Pro	Lys	Ala	Val	Pro	Glu	Val	Gln	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val

[illegible]

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<210> 43
<211> 660
<212> DNA
<213> Homo Sapiens
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<220>
<221> CDS
<222> (1) ... (660)
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<400> 43																
atg	gcg	tgg	agt	ctt	ggg	agc	tgg	ctg	ggt	ggc	tgc	ctg	ctg	gtg	tca	48
Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser	
1				5					10					15		
gca	ttg	gga	atg	gta	cca	cct	ccc	gaa	aat	gtc	aga	atg	aat	tct	gtt	96
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	
			20					25					30			
aat	ttc	aag	aac	att	cta	cag	tgg	gag	tca	cct	gct	ttt	gcc	aaa	ggg	144
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	
		35					40					45				
aac	ctg	act	ttc	aca	gct	cag	tac	cta	agt	tat	agg	ata	ttc	caa	gat	192
Asn	Leu	Thr	Phè	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	
	50					55					60					
aaa	tgc	atg	aat	act	acc	ttg	acg	gaa	tgt	gat	ttc	tca	agt	ctt	tcc	240
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	
65					70					75					80	
aag	tat	ggg	gac	cac	acc	ttg	aga	gtc	agg	gct	gaa	ttt	gca	gat	gag	288
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	
				85					90					95		
cat	tca	gac	tgg	gta	aac	atc	acc	ttc	tgt	cct	gtg	gat	gac	acc	att	336

His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
			100					105					110			
att	gga	ccc	cct	gga	atg	caa	gta	gaa	gta	ctt	gat	gat	tct	tta	cat	384
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
		115					120					125				
atg	cgt	ttc	tta	gcc	cct	aaa	att	gag	aat	gaa	tac	gaa	act	tgg	act	432
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	
	130					135					140					
atg	aag	aat	gtg	tat	aac	tca	tgg	act	tat	aat	gtg	caa	tac	tgg	aaa	480
Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	
145					150					155					160	
aac	ggt	act	gat	gaa	aag	ttt	caa	att	act	ccc	cag	tat	gac	ttt	gag	528
Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	
				165					170					175		
gtc	ctc	aga	aac	ctg	gag	cca	tgg	aca	act	tat	tgt	gtt	caa	gtt	cga	576
Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	
			180					185					190			
ggg	ttt	ctt	cct	gat	cgg	aac	aaa	gct	ggg	gaa	tgg	agt	gag	cct	gtc	624
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val	
		195					200					205				
tgt	gag	caa	aca	acc	cat	gac	gaa	acg	gtc	ccc	tcc					660
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser					
	210					215					220					

<210> 44  
 <211> 220  
 <212> PRT  
 <213> Homo Sapiens

<400> 44

Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser	
1				5					10					15		
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	
			20					25					30			
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	
		35				40					45					
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	
	50					55					60					
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	
65				70						75					80	
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	
				85					90					95		
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
			100					105					110			
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
		115					120					125				
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	
	130					135					140					
Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	
145					150					155					160	
Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	
				165					170					175		
Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	
			180					185					190			
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val	
		195					200					205				
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser					
	210					215					220					

<210> 45  
 <211> 199  
 <212> PRT  
 <213> homo sapiens

<400> 45  
 Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys  
 1 5 10 15  
 Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr  
 20 25 30  
 Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met  
 35 40 45  
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly  
 50 55 60  
 Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp  
 65 70 75 80  
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro  
 85 90 95  
 Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe  
 100 105 110  
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn  
 115 120 125  
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr  
 130 135 140  
 Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg  
 145 150 155 160  
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu  
 165 170 175  
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln  
 180 185 190  
 Thr Thr His Asp Glu Thr Val  
 195

<210> 46  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe  
 1 5 10 15  
 Glu Ala Glu Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn  
 20 25 30  
 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile  
 35 40 45  
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp  
 50 55 60  
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala  
 65 70 75 80  
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr  
 85 90 95  
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val  
 100 105 110  
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro  
 115 120 125  
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser  
 130 135 140  
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe  
 145 150 155 160  
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr  
 165 170 175  
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala  
 180 185 190

Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu  
 195 200 205  
 Thr Arg Gln  
 210

<210> 47  
 <211> 201  
 <212> PRT  
 <213> homo sapiens

<400> 47  
 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
 1 5 10 15  
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly  
 20 25 30  
 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu  
 35 40 45  
 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu  
 50 55 60  
 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr  
 65 70 75 80  
 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser  
 85 90 95  
 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro  
 100 105 110  
 Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu  
 115 120 125  
 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu  
 130 135 140  
 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro  
 145 150 155 160  
 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala  
 165 170 175  
 Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr  
 180 185 190  
 Glu Cys Val Glu Val Gln Gly Glu Ala  
 195 200

<210> 48  
 <211> 68  
 <212> PRT  
 <213> Mus musculus

<400> 48  
 His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln  
 1 5 10 15  
 Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser  
 20 25 30  
 Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg  
 35 40 45  
 Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys  
 50 55 60  
 Asn Leu Thr Met  
 65

<210> 49  
 <211> 26  
 <212> PRT  
 <213> mus musculus

<400> 49  
 Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val  
 1 5 10 15

Ser Ala Gly Gly Pro Pro Val Thr Lys Met  
                   20                                  25

<210> 50  
 <211> 28  
 <212> PRT  
 <213> mus musculus

<400> 50  
 Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp  
   1                  5                                  10                  15  
 Val Thr Cys Ile Pro Lys Val Arg Ser Ile Gln Met  
                   20                                  25

<210> 51  
 <211> 40  
 <212> PRT  
 <213> Mus musculus

<400> 51  
 Leu Val His Pro Thr Leu Thr Pro Val Leu Ser Glu Asp Gly His Gln  
   1                  5                                  10                  15  
 Leu Thr Leu Glu Glu Ile Phe His Asp Leu Phe Tyr Arg Leu Glu Leu  
                   20                                  25                  30  
 His Val Asn His Thr Tyr Gln Met  
                   35                                  40

<210> 52  
 <211> 50  
 <212> PRT  
 <213> Mus musculus

<400> 52  
 His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro  
   1                  5                                  10                  15  
 Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile Leu Ser  
                   20                                  25                  30  
 Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro Leu Val  
                   35                                  40                  45  
 Pro Arg  
           50

<210> 53  
 <211> 70  
 <212> PRT  
 <213> Mus musculus

<400> 53  
 His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro  
   1                  5                                  10                  15  
 Asp Thr Glu Phe His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu  
                   20                                  25                  30  
 Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr  
                   35                                  40                  45  
 Pro Ile Leu Ser Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr  
                   50                  55                  60  
 Leu Pro Leu Val Pro Arg  
   65                                  70

<210> 54  
 <211> 46

<212> PRT

<213> Mus musculus

<400> 54

Glu	Thr	Arg	Asn	His	Thr	Glu	Phe	Tyr	Tyr	Ala	Lys	Val	Thr	Ala	Val
1				5					10					15	
Ser	Ala	Gly	Gly	Glu	Thr	Arg	Asn	His	Thr	Glu	Phe	Tyr	Tyr	Ala	Lys
		20					25					30			
Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	Pro	Pro	Val	Thr	Lys	Met		
		35				40						45			

<210> 55

<211> 48

<212> PRT

<213> mus musculus

<220>

<221> VARIANT

<222> 6, 11, 13,

<223> Xaa = Any Amino Acid

<400> 55

Thr	Asp	Arg	Phe	Ser	Xaa	Leu	Gln	His	Thr	Xaa	Ile	Xaa	Pro	Xaa	Asp
1				5					10					15	
Xaa	Xaa	Xaa	Ile	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Ile
		20					25					30			
Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Pro	Lys	Val	Arg	Ser	Ile	Gln	Met
		35				40						45			

<210> 56

<211> 92

<212> PRT

<213> homo sapiens

<400> 56

Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser	Ser
1				5					10					15	
Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	Pro
		20					25					30			
Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	Trp
		35				40					45				
Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu
	50				55					60					
Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr
65				70				75						80	
Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met				
				85				90							

<210> 57

<211> 28

<212> PRT

<213> Homo sapiens

<400> 57

Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp
1				5					10					15	
Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met				
		20					25								

<210> 58

<211> 40

<212> PRT

<213> Homo sapiens

<400> 58

```

Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg
 1          5          10          15
Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu
          20          25          30
Gln Val Asn Arg Thr Tyr Gln Met
          35          40

```

<210> 59

<211> 25

<212> PRT

<213> Homo sapiens

<400> 59

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His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 1          5          10          15
Asp Thr Glu Phe Leu Gly Thr Ile Met
          20          25

```

<210> 60

<211> 14

<212> PRT

<213> Homo sapiens

<400> 60

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Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met
 1          5          10

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<210> 61

<211> 12

<212> PRT

<213> Homo sapiens

<400> 61

```

Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr
 1          5          10

```

<210> 62

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> A murine IL-22RA soluble receptor with cleavage site (Leu Val Pro Arg) remaining on C-Terminus

<400> 62

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His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln
 1          5          10          15
Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser
          20          25          30
Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg
          35          40          45
Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys
          50          55          60
Asn Leu Thr Met Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys
65          70          75          80
Val Thr Ala Val Ser Ala Gly Gly Pro Pro Val Thr Lys Met Thr Asp
          85          90          95
Arg Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp Val Thr

```



[illegible]